

A dashed-line outline of the word "GO" in a stylized, blocky font. The outline consists of several thick, horizontal and vertical lines forming the letters. To the right of the outline, the registered trademark symbol (TM) is placed vertically.

Database:	EST-STS-THREE
1/4:EST113	1/6:EST116
1/6:EST116	1/7:EST117
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1/199:EST309	1/200:EST310

Release 2.1D John F. Collins' Biocomputing Research Unit.
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Statistics: Mean 11.349; Variance 2.120; scale 5.35

tabular output not generated.

Scoring table: TABLE default.

Nmatch : Dbase 0; Query 0
Searched : 887282 seqs, 320523884 bases x 2
Post-processing: Minimum Match 0%
Listings first 45 summaries

Database: EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
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Database: EST99
EST-EST-Two

100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109

BEST AVAILABLE COPY

Database: EST-STS-TREE
 175:EST175 176:EST176 177:EST177 178:EST178 179:EST179
 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184
 185:EST185 186:EST186 187:EST187 188:EST188 189:EST189
 190:EST190 191:EST191 192:EST192 193:EST193
 EST-STS-TREE
 194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6
 200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12
 206:ueEST 207:gnEST1 208:gnEST2 209:gnEST3 210:gnEST4
 211:gnEST5 212:gnEST6 213:gnEST7 214:gnEST8 215:gnEST9
 216:gnEST10 217:gnEST11 218:gnEST12 219:gnEST13
 220:gnEST14 221:gnEST15 222:gnEST16 223:gnSTS 224:enEST1
 225:enEST 226:enEST 227:enEST 228:enEST5 229:enEST6
 230:enEST7 231:enEST8 232:enEST9 233:enEST10 234:enEST11
 235:enEST12 236:enEST13 237:enEST14 238:enEST15
 239:enEST16 240:enEST17 241:enEST18 242:enEST19
 243:enEST20 244:enEST21 245:enEST22 246:enEST23
 247:enEST24 248:enEST25 249:enEST26 250:enEST27
 251:enSTS
 Statistics:
 Mean 11.349; Variance 2.120; scale 5.354
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description	Pred.	No.
C	1	33	2.1	451	197	N40913	human STS CHIC.ATC1.P	3.12e-18	
C	2	32	2.0	231	81	N43925	yf45900..1 Homo sapi	1.7e-15	
C	3	31	2.0	239	97	G08851	human STS CHIC.ATC3C1	3.44e-15	
C	4	31	2.0	255	51	PCU04650	Parachartergus colobo	3.44e-15	
C	5	31	2.0	255	205	PCU04650	Parachartergus colobo	3.44e-15	
C	6	31	2.0	255	204	PCU04650	Parachartergus colobo	3.44e-15	
C	7	31	2.0	256	196	G08117	human STS CHIC.ATC3E0	3.44e-15	
C	8	31	2.0	298	203	HS2346YB5	H. sapiens (DLS781) D	3.44e-15	
C	9	32	2.0	314	197	G08919	human STS CHIC.ATC6.P	1.07e-16	
C	10	31	2.0	377	197	G02533	human STS CHIC.ATC2F0	3.44e-15	
C	11	31	2.0	514	193	ATT0025	A. thaliana transcript	3.44e-16	
C	12	32	2.0	521	205	HUM077996	Human STS UTR996.	1.07e-16	
C	13	32	2.0	521	204	HUM077996	Human STS UTR7996.	1.07e-16	
C	14	31	2.0	588	197	G09471	Human STS CHIC.ATC5A0	3.44e-16	
C	15	30	1.9	277	197	G09999	human STS CHIC.GC116B	1.04e-13	
C	16	30	1.9	311	197	G10330	human STS CHIC.ATC7F0	1.04e-13	
C	17	30	1.9	326	205	HUM078005B	Human STS UTR8005, 3'	1.04e-13	
C	18	30	1.9	326	204	HUM078005B	Human STS UTR8005, 3'	1.04e-13	
C	19	30	1.9	332	197	G02526	human STS CHIC.ATC3C1	1.04e-13	
C	20	30	1.9	334	197	G10329	human STS CHIC.ATC6F1	1.04e-13	
C	21	30	1.9	339	197	G09361	human STS CHIC.ATC2F0	1.04e-13	
C	22	30	1.9	342	204	HUM077997	Human STS UTR7997.	1.04e-13	
C	23	30	1.9	342	205	HUM077997	Human STS UTR7997.	1.04e-13	
C	24	30	1.9	345	197	G09257	human STS CHIC.ATC2B1	1.04e-13	
C	25	30	1.9	359	104	R23641	yh35E02..1 Homo sapie	1.04e-13	
C	26	30	1.9	366	204	HUM071040	Human STS UTR040.	1.04e-13	
C	27	30	1.9	366	205	HUM071040	Human STS UTR040.	1.04e-13	
C	28	30	1.9	366	196	G08221	human STS CHIC.ATC3A0	1.04e-13	
C	29	30	1.9	372	22	HSPD03455	H. sapiens EST sequenc	1.04e-13	
C	30	30	1.9	372	22	HSPD03455	human STS CHIC.ATC2D1	1.04e-13	
C	31	30	1.9	395	197	G08663	human STS CHIC.ATC2B1	1.04e-13	
C	32	30	1.9	397	197	G09348	human STS CHIC.ATC2B1	1.04e-13	
C	33	30	1.9	403	97	G09245	human STS CHIC.ATC2C0	1.04e-13	
C	34	30	1.9	407	54	H85715	Y868906..1 Homo sapi	1.04e-13	
C	35	30	1.9	416	92	M78226	EST00444 Homo sapiens	1.04e-13	
C	36	30	1.9	444	204	HUM07615	Human STS UTR6615.	1.04e-13	
C	37	30	1.9	444	205	HUM07615	Human STS UTR6615.	1.04e-13	
C	38	30	1.9	521	140	R76563	y166a07..1 Homo sapi	1.04e-13	
C	39	29	1.9	554	199	H91490	SMWRC073JSK Brugia ma	2.97e-13	
C	40	1.9	559	198	G15456	Human STS CHIC.ATC5H0	1.04e-13		
C	41	30	1.9	588	197	G09469	human STS CHIC.ATC4C0	1.04e-13	
C	42	30	1.9	625	197	G09478	human STS CHIC.ATC4D0	1.04e-13	
C	43	30	1.9	634	205	HUM076229	Human STS UTR6629.	1.04e-13	

ALIGNMENTS

RESULT 1
LOCUS G09413 451 bp DNA
DEFINITION human STS CHLC.ATCL.P9551 clone ATCL.
ACCESSION G09413
NID 94126
KEYWORDS NTS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XI individual of French nationality.

REFERENCE
AUTHORS Homo sapiens
TITLE Euaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
JOURNAL

COMMENT
 1 (bases 1 to 451)
 Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Buetow,K.H.
 Cooperative Human Linkage Center
 Unpublished (1995)
 Synonyms: ATCL, CHLC.ATCL.T9550
 GDB: 600-365-092
 Contact: Dr. Jeffrey C. Murray
 The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 335-3508
 Fax: (319) 336-3347
 Email: jeff-murray@uiowa.edu

PRIMER A: CATCACCACTGTACCCATCA
PRIMER B: CCATGGCCTAGCAATTG

PCR Profile:
STS size: 133
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extenstion: 6 minutes at 72 degrees C

Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.

FEATURES
source
STS
primer_bind
primer_bind
location/Qualifiers
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 /organism="Homo sapiens"
 169..301
 169..188
 primer_bind complement(282..301)
BASE COUNT 134 a 92 c 78 g 137 t 10 others
ORIGIN

Query Match 2.1%; Score 33; DB 197; Length 451;
Best Local Similarity 97.1%; Pred. No. 3..12e-18;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 245 catcatcatcatcatcatcatcatcacaacag 279
Oy 7 CATCATCATCATCATCATCATCACAGCAG 41

RESULT 3
LOCUS G08851 239 bp DNA
DEFINITION human STS CHLC.ATC3C12.P7566 clone ATC3C12.
ACCESSION G08851
NID 939401
KEYWORDS NTS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XI individual of French nationality.
ORGANISM Homo Sapiens
 Euaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
COMMENT
 Homo sapiens-276546 primer=p77 library=Soares multiple sclerosis RI sites of a modified pT7 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NIH/NINDS).
ORGANISM
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
 1 (bases 1 to 231)
 Hillier,L., Clark,N., Dubuge,T., Elliston,K., Hawkins,M., Holman,M., Holtzman,M., Kucaba,T., Lennon,G., Marra,M., Parsons,J., Rikoff,L., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE
JOURNAL
 unpublished (1995)
COMMENT
 Contact: Wilson RR
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8301, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 183
Source: IMAGE Consortium, LInN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
This clone is available royalty-free through LInN ; contact the Location/Qualifiers

1..231
 /organism="Homo sapiens"
 /clone="276546"
 /clone="276546"

FEATURES
source
mRNA
BASE COUNT 65 a 43 c 41 g 80 t 2 others
ORIGIN

Query Match 2.0%; Score 32; DB 81; Length 231;
Best Local Similarity 90.0%; Pred. No. 1.07e-16;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 137 gctatccatcatcatcatcatcatcatccctcgatcg 176
Oy 5 GCCATCATCATCATCATCATCATCACACGAGCG 44

RESULT 3
LOCUS G08851 239 bp DNA
DEFINITION human STS CHLC.ATC3C12.P7566 clone ATC3C12.
ACCESSION G08851
NID 939401
KEYWORDS NTS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XI individual of French nationality.
ORGANISM Homo Sapiens
 Euaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

RESULT 2
ORGANISM

ACCESSION	U64650	NID	91495941	annealing:	75 seconds at 55 degrees C
NID		STS.		extension:	15 seconds at 72 degrees C
SOURCE	Parachartergus colobopterus	Protocol:		PCR cycles:	27
ORGANISM	Parachartergus colobopterus	Template:	30ng genomic DNA		
Eukaryota; mitochrondrial eukaryotes; Metazoa: Arthropoda;	Primer:	each 1.5 pmole			
Aculeata; Vespoidea; Vespidae; Polistinae; Parachartergus.	dNTPs:	0.3 units			
Tracheata; Hexapoda; Insecta; Pterygota; Hymenoptera; Apocrita;	Tag Polymerase:	200 uM			
1 (bases 1 to 25)	Total Vol:	10 ul			
Strassmann,J.E., Solis,C.R., Barefield,K. and Queller,D.C.					
trinucleotide microsatellite loci in a swarm-founding neotropical					
wasp, Parachartergus colobopterus and their usefulness in other					
social wasps					
Mol. Ecol. 5 (3), 459-461 (1996)					
JOURNAL		Buffer:			
MEDLINE		MgCl2: 1.5mM			
REFERENCE	96266704	KCl: 50mM			
AUTHORS	2 (bases 1 to 255)	Trits: 10mM			
TITLE	Strassmann,J.E., Hughes,C.R., Barefield,K., Solis,C.R. and	pH: 8.3.			
JOURNAL	Queller,D.C.				
FEATURES	Direct Submission				
source	Submitted (19-JUL-1996) Ecology & Evolutionary Biology, Rice				
satellite	1..255	/organism="Parachartergus colobopterus"			
primer_bind	1..255	/clone=Pacc3301CA"			
repeat_region	1..208				
prime_bind	236..255				
BASE COUNT	59 a 57 c 90 g 49 t				
ORIGIN					
RESULT	7	Query Match	2.0%		
DEFINITION	human STS CHLC.ATC3E01.P7574 clone ATC3E01.	Score	31;		
ACCESSION	G08117	DB	204;		
NID	993867	Length	255;		
KEYWORDS	STs sequence; primer; sequence tagged site.	Pred. No.	3.44e-15;		
ORGANISM	genomic DNA prepared from XY individual of French nationality.	Mismatches	0;		
Bukaryota; mitochondrial eukaryotes; Metazoa; Chordata;	Indels	0;			
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;	Gaps	0;			
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;					
Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 256)	RESULT	8		
AUTHORS	Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Buetow,K.H.	LOCUS	HSB346YB5		
TITLE	unpublished (1995)	DEFINITION	H.sapiens (DLS281) DNA segment containing (CA) repeat; clone		
JOURNAL	Synonyms: ATC3E01, CHLC.ATC3E01.#T7573	ACCESSION	ARMb346yb5; single read.		
COMMENT	Contact: Dr. Jeffrey C. Murray	NID	91235224		
DoIT		KEYWORDS	CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; SIS.		
The University of Iowa		SOURCE	human.		
Department of Pediatrics, Iowa City, IA 52242, USA		ORGANISM	Homo sapiens		
Tel: (319) 356-3508		REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
Fax: (319) 356-3347		AUTHORS	1 (bases 1 to 298)		
Email: jeff.murray@uiowa.edu		TITLE	Weissenbach,J.		
Primer A: GCTGGATGATAAATGCTT		JOURNAL	Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.		
Primer B: AAATGCCACTCCCTAAAC		REFERENCE	E-mail: Jean.Weissenbach@genethon.fr		
STS size: 147		AUTHORS	2 (bases 1 to 298)		
PCR Profile:		TITLE	dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyabay,G., Morissette,J. and Weissenbach,J.		
denature: 30 seconds at 94 degrees C		JOURNAL	A comprehensive genetic map of the human genome based on 5,264 microsatellites		
		MEDLINE	Nature 380 (6570), 152-154 (1996)		
		COMMENT	96176476		
		FEATURES	full automatic.		
		source	Location/Qualifiers		
			1..298		
			/organism="Homo sapiens"		
			/note="cloning vector is M13mp18"		
			/cell_line="CPH 134702"		
			/clone.lib="genomic DNA"		
			/chromosome="1"		
		BASE COUNT	90 a 107 c 33 g 66 t		
		ORIGIN	2 others		
		Query Match	2.0%		
		Best Local Similarity	97.0%		
		Matches	32;		
		Conservative	1;		
		Mismatches	0;		
		Indels	0;		
		Gaps	0;		

SOURCE	Arabidopsis thaliana
ORGANISM	Eukaryota; mitochondrial eukaryotes; Viridiplantae; Charophytidae/Embryophyta group; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 514)
AUTHORS	Quigley and Mache, R.
TITLE	Direct Submission
JOURNAL	Submitted (10-AUG-1993) CNRS, GDR-1003 ACS, INRA, laboratoire de Biologie Moléculaire, Bp 27, 31326 Castanet-Tolosan cedex, France. E-mail:gdr-sv@eteleuse.inra.fr. On behalf of: CNRS URA 1178, Laboratoire de Biologie Moléculaire végétale, B.P. 53X, 38041 Grenoble Cedex, France. E-mail:FQUIGLEY@grenet.fr
COMMENT	CNRS. The Arabidopsis thaliana transcribed genome: the GDR cDNA program Cloning vector: Lambda ZAPII.; full automatic.
FEATURES	Location/Qualifiers
SOURCE	1..514
ORIGIN	/organism="Arabidopsis thaliana" 'clone'="GBGe87" 'tissue-type'="Flower buds of A.thaliana ecotype columbia C24" 'clone.lib'="Grenoble-B"
BASE COUNT	153 a 101 c 114 g 146 t
RESULT	12
LOCUS	HUMUT7996
DEFINITION	521 bp
ACCESSION	DNA
NID	STS
KEYWORDS	Best Local Similarity 2.0%; Score 31; DB 19; Length 514; Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	431 atccatcatcatcatcatcatcatcatca 463
Qy	8 ATCATCATCATCATCATCATCATCACAGCA 40
RESULT	13
LOCUS	HUMUT7996
DEFINITION	521 bp
ACCESSION	DNA
NID	STS
KEYWORDS	PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; trinucleotide repeat.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 521) Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and White,R.
TITLE	Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
JOURNAL	Unpublished (1994)
COMMENT	Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics Salt Lake City, UT 84112
FEATURES	Location/Qualifiers
SOURCE	1..521
ORIGIN	/organism="Homo sapiens"
BASE COUNT	103 a 163 c 103 g
RESULT	14
LOCUS	HUMUT7996
DEFINITION	521 bp
ACCESSION	DNA
NID	STS
KEYWORDS	Best Local Similarity 2.0%; Score 32; DB 204; Length 521; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	207 ggccatcatcatcatcatcatcatca 238
Qy	4 GGCCATCATCATCATCATCATCATCA 35
RESULT	15
LOCUS	HUMUT7996
DEFINITION	521 bp
ACCESSION	DNA
NID	STS
KEYWORDS	PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; trinucleotide repeat.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 521) Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and White,R.
TITLE	Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
JOURNAL	Unpublished (1994)
COMMENT	Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics Salt Lake City, UT 84112
FEATURES	Location/Qualifiers
SOURCE	1..521
ORIGIN	/organism="Homo sapiens"
BASE COUNT	103 a 163 c 103 g
RESULT	16
LOCUS	HUMUT7996
DEFINITION	521 bp
ACCESSION	DNA
NID	STS
KEYWORDS	Best Local Similarity 2.0%; Score 32; DB 204; Length 521; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	207 ggccatcatcatcatcatcatcatca 238
Qy	4 GGCCATCATCATCATCATCATCA 35



RESULT 3
ID R76528 standard; Protein: 170 AA.
AC R76528;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cafl (F1) antigen.
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
DB 302 nsaeelnrnfqkydsvmqrlldtsqk 329
QQ 494 NSATEALNRFPIQKSYDSMORLIDDSGK 521

RESULT 2
ID R79962 standard; Protein: 329 AA.
AC R79962;
DT 18-APR-1996 (first entry)
DE Partial lcrv (V antigen) of Y. pestis.
KW lcrv; V antigen; virulence; plague; vaccine; epitope.
OS Yersinia pestis.
PN WO9524475-A1.
PD 14-SEP-1995.
PR 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-00457.
PA (MINA) UK SEC FOR DEFENCE.
PT Leary SEC, Titball RW, Williamson ED, Leary SE;
DR WPI: 95-328268/42.
DR N-PSDB; 104223.

PT Recombinant DNA expressing Yersinia pestis V antigen - useful in oral or parenteral vaccines for protection against plague
PS Claim 6; Page 15-16; 25pp; English.
CC R79961-62 are encoded by T04222-23 (resp.), DNA sequences (lcrv) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione-S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (lcrv) is an unstable 37 kDa monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.
SQ Sequence 329 AA;

Query Match 63.0%; Score 2233; DB 15; length 329;
Best Local Similarity 99.4%; Pred. No. 1: 80e-163;
Matches 323; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 5 irayeqnphifedekvrgveqltgghssvleelqvlvkdknidsikyprkssevfan 64
QQ 197 IRAYEONPQHPIEDEKVRYQVLTGHGSVLEELVOLVKDKNIDIKYPRKSEVFAN 256

Db 65 rvtddekkklaylpdedaikgkhgdyqlqgikrkeflssspntqwearfamv 124
QQ 257 RVTDDEKKKKLAYLPDEDAIKGKHGDYQLQGIKRKFLSSSPNTQWEARFAMV 316

Db 125 mhfsldtriddikkvivdmnhgdaaskrlreelaqtaekiyvsigainkhiss 184
QQ 317 NHFSLTADRIDDDILKIVDWSMNHHGDASKRLREELAELTAEKIYVSIGAEINKHSS 376

Db 185 gtnihdksinlmknlygtdeikasaykilekmpgtiqdgskekivskdfg 244
QQ 377 GTINIHDKSINLMKNLYGYDEIKASAYKILEKMPGTIQDGSERKIVSKDFG 436

Db 245 senkrtgalgnknsysynkdnelshtattcsdrplndvskttqslsditrrnsa 304
QQ 437 SENKRTGALGNKNSYSYNKDNLSELHSHATTCSDRPLNDVSKTTQSLSDITRNSA 495

Db 305 iealnrfqkydsvmqrlldtsqk 329
QQ 497 IEALNRFIQKSYDSMORLIDDSGK 521

RESULT 3
ID R76526 standard; Protein: 170 AA.
AC R76526;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cafl (F1) antigen.
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
DB 171 pkvngenlvddvvlatgssffvrsigshgklaagkytdavtvtsq 170
QQ 144 PKVNGENLVDDVVLATGSSFFVRSIGSHGKLAAGKYTDAVTVTSQ 193

RESULT 4
ID R76526 standard; Protein: 151 AA.
AC R76526;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cafl (F1) antigen.
KW Yersinia pestis; Salmonella typhimurium; Salmonella typhi; bubonic plague; pneumonic plague.
OS Yersinia pestis.
DB 200 05-JUL-1995.
PR 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PT Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 95-246396732.
DR N-PSDB; Q92817.
PT DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response, against Yersinia pestis, at mucosal surfaces.
PS Disclosure; Page 16; 27pp; English.
CC The sequence represents the Y. pestis cafl (F1) antigen expressed from plasmid pGAL2. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. Pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.
SQ Sequence 170 AA;

Query Match 31.0%; Score 1100; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.61e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkkssviaalfqtiataanaditasttattatativeparitivitykegapitindngnidt 60
QQ 24 MRKISSVIAALFGTIATAADUITASTTATATIVEPARTITLTYKEGAPITIMGNIDT 83

Db 61 ellvgltiqgkgttstsvnftdaagpmlyiftsgqgnhafttkvgkdsfdas 120
QQ 84 ELLVGLTIQGKGTTSVNFDTDAAGPMLYIFTSGQGNHAFTTKVGKDSFDAS 143

bioavailability 5- to 100-fold. The agent and bacterial protein may be linked via a degradable peptide sequence as a fusion protein. The receptor binding region of the invasin protein involves the 192 amino acids at the C-terminal end of the protein. This region retains the binding affinity of the protein, and may be used alone or as part of a fusion protein for drug delivery. The binding region may be fused with maltose binding protein (R96209) which may be purified easily by to form a fusion protein (R96209) which may be purified easily by amylose affinity chromatography. The delivery system allows improved transport across enterocytes and Peyer's patch M-cells. The system is not prone to degradation in the gut or early release of biologically active material, and eliminates the need for parenteral administration.

Sequence 835 AA;

Query Match 3.1%; Score 110; DB 17; Length 835;
Best Local Similarity 25.8%; Prod. No. 9.84e+00; ID R57771 standard; Protein: 455 AA.
Matches 33; Conservative 43; Mismatches 42; Indels 10; Gaps 8; PR 30-OCT-1990; JP-294055.
Db 509 qvisiisltstfvgvsvtldiqgqgatvdvrfaalppdvtnsfpsdivasamsqi 568 PA (MITK) MITSUI TOATSU CHEM INC.
Qy 29 SVAIALFG-TIATANNA-DLTAS-TITATATL-VEPARITYKEGAPTRIMDNGNIDTE 84 PA (YOSH-) YOSHIYUKI KANAI GH.
DR WPI: 94-07375/10.
Db 569 ltfvpkrknnefvsgitd-liefqs-gpvptispytenadn--vsavsgvngsfdvit 623 PT Anti-DNA antibody prodn. augmenting factor - and antibodies to disclosure; Fig 7; 29pp; Japanese.
Qy 85 L-LVGLTLLGGYKTGTTSVNFDAAGDPMLTFTSDQGNHHQFTTKVIGKDSRDFDIS 143 PS Nuc protein binds DNA and augments anti-DNA antibody prodn. The CC Nuc protein binds DNA and augments anti-DNA antibody prodn. The CC protein is from human or mouse tissue or cells, esp. lymphocytes. CC Anti nuc protein antibodies may be used to treat diseases involving CC prodn. of large amts. of DNA binding protein, e.g. autoimmune disease.

Qy 144 PKYNGENI 151
Sequence 455 AA;

Query Match 3.0%; Score 108; DB 10; Length 455;

Best Local Similarity 19.8%; Prod. No. 1.30e-01; ID R13992 standard; Protein: 493 AA.

Matches 36; Conservative 57; Mismatches 82; Indels 7; Gaps 7; PR 21-SEP-1994 (first entry)

Db 223 sqaqikveeweldgdpnrtpktffilhainsqvdgvdqcealealftkelykvdkpnee 282 DE P. falciparum sporozoite antigen fusion polypeptide.

Qy 344 ARSKREELAELLA-ELKIVSIVGEINKHLSSGTINHD-KSINTMD-KNLYGYTBEE 400 KW Vaccine; NYX gene; malaria; antibodies; purification; affinity.

Db 283 dmreeneerlrmrehvmkvudnadrlnvlteeflastgrkerqdtgeowktvmspayt 342 OS Plasmodium falciparum.

Qy 401 IFKASLEYKILEKMQTIQVGDGSEKKVKSIEKGLENSENKRRT-GALGN-LKN-SYSYNKD 457 FT Key Region 1.21

Db 343 eeelkkfeefeaareaelna-raqrslsqealqrsqrdrleaqkrelggmegrkqqlqeq 401 FT Label= A

Qy 458 NNELSHFATTCSDSRPLNDVSQRTQTLSDITSRFSNAEALNRFIQKWDSDWMRLDD 517 FT Notes "affinity peptide including 6 His residues"

Db 402 sa 403
Qy 518 TS 519

Query Match 3.0%; Score 106; DB 17; Length 174;
Best Local Similarity 34.5%; Prod. No. 1.70e+01; ID R13991 standard; Protein: 493 AA.

Matches 20; Conservative 12; Mismatches 24; Indels 2; Gaps 2; PR 25-MAR-1991; 103920.

Query Match 3.0%; Score 106; DB 17; Length 174;
Best Local Similarity 34.5%; Prod. No. 1.70e+01; ID R13991 standard; Protein: 493 AA.

Matches 20; Conservative 12; Mismatches 24; Indels 2; Gaps 2; PR 25-MAR-1991; 103920.

PR	23-MAR-1990; CH-000970.	FT	Region	162..166
PA	(HOFF) HOFFMANN-LA ROCHE AG.	FT	/Label= conserved sequence in RU6	
PI	Corta U, Guttinger M, Matile H;	FT	Region	647..651
WPI;	91-282898/39.	FT	/Label= conserved sequence	
PT	New antimalarial polypeptide(s) - corresp. to specific epitope(s)	FT	/note= "homologous to sequences	
PT	of the Plasmodium falciparum sporozoite antigen, and are useful as vaccines or to prepare antigens	PN	WO9103030-A.	
PS	Claim 2; Page 18; 36PP; German.	PD	18-OCT-1990; U01678.	
CC	vector PDS56/RBSII_6xHis is a derivative of pDS56/RBS (EP-282042).	PF	30-MAR-1990.	
CC	It comprises an additional sequence encoding six histidine residues.	PR	06-APR-189; US-335178.	
CC	into this vector may be ligated a 1400 bp Asel fragment of NXY (see 013727) to yield pDS-NXY. E. coli SG13009 (pUHAT) transformed with pDS-NXY produces a 69 kD fusion protein comprising the NXY	PA	(UNIW) Washington State University.	
CC	units, and C-terminally to a vector-derived sequence.	PI	McGuire TC, Palmer GH, Barbett AF, Davis MC, Allred DR.	
CC	fragment B corresponds to amino acids 1-462 of the N-terminal of the sporozoite antigen. The affinity peptide is used for the purification of the antigen. The polypeptide is useful for the prodn. of antimalarial vaccines.	DR	WPI; 90-313801/44.	
CC	See also 013727-8.	DR	N-PADB; Q07041.	
CC	Sequence 493 AA;	PT	Rickettsial antigens for vaccination and diagnosis - comprise	
CC	Best local Similarity 21.6%; Pred. No. 1.95e-01; Length 493; Matches 16; Conservative 19; Mismatches 38; Indels 1; Gaps 1;	PT	specified amino acid sequences derived from purified surface	
Db	5 hhbbhbgsynsynkennnnkknnkvavkhinavdkvavnkvnkvnktvsklav 64	PS	proteins of Anaplasma marginale.	
OS	: : :::: : : ; : ; ::	CC	Antigens raised to the repeated peptide epitopes encoded by the DNA	
QY	7 HHHHHHSQGHDDDKHKMKKISSVIAIALFGTTATANAADLTASITATATIVEPARITLT 66	CC	preferred are peptides from the following sequence which include the peptide in parentheses:	
Db	65 ykvns-vhkmnavn 77	CC	ADSSASGQEQESSVSQS-[EASTSS]-QLG	
Qy	67 YKEGAPITMDNGN 80	CC	See also R08401-R08405.	
RESULT	11	SQ	Sequence 708 AA;	
ID	R08402 standard; Protein; 708 AA.	CC		
AC	ACR08402;	CC		
DT	16-MAY-1991 (first entry)	CC		
DE	Am105 encoded by Idaho allele of the MSP-1a gene.	CC		
KW	rickettsial antigen; vaccine; major surface protein-1; Am105.	CC		
OS	Anaplasma marginale.	CC		
FH	Location/Qualifiers	CC		
FT	Region 10..183	CC		
FT	/label= repeat region 10..38	CC		
FT	/label= repeat unit 1	CC		
FT	/note= "tandem"	CC		
FT	Region 16..20	CC		
FT	/label= conserved sequence in RU1	CC		
FT	Region 30..68	CC		
FT	/label= repeat unit 2	CC		
FT	/note= "tandem"	CC		
FT	Region 45..49	CC		
FT	/label= conserved sequence in RU2	CC		
FT	Region 69..97	CC		
FT	/label= repeat unit 3	CC		
FT	/note= "tandem"	CC		
FT	Region 75..79	CC		
FT	/label= conserved sequence in RU3	CC		
FT	Region 98..126	CC		
FT	/label= repeat unit 4	CC		
FT	/note= "tandem"	CC		
FT	Region 104..108	CC		
FT	/label= conserved sequence in RU4	CC		
FT	Region 127..155	CC		
FT	/label= repeat unit 5	CC		
FT	/note= "tandem"	CC		
FT	Region 133..137	CC		
FT	/label= conserved sequence in RU5	CC		
FT	Region 156..183	CC		
FT	/label= repeat unit 6	CC		
FT	/note= "tandem"	CC		
PR	23-MAR-1990; CH-000970.	FT	Region	162..166
PA	(HOFF) HOFFMANN-LA ROCHE AG.	FT	/Label= conserved sequence in RU6	
PI	Corta U, Guttinger M, Matile H;	FT	Region	647..651
WPI;	91-282898/39.	FT	/Label= conserved sequence	
PT	New antimalarial polypeptide(s) - corresp. to specific epitope(s)	FT	/note= "homologous to sequences	
PT	of the Plasmodium falciparum sporozoite antigen, and are useful as vaccines or to prepare antigens	PN	WO9103030-A.	
PS	Claim 2; Page 18; 36PP; German.	PD	18-OCT-1990; U01678.	
CC	vector PDS56/RBSII_6xHis is a derivative of pDS56/RBS (EP-282042).	PF	30-MAR-1990.	
CC	It comprises an additional sequence encoding six histidine residues.	PR	06-APR-189; US-335178.	
CC	into this vector may be ligated a 1400 bp Asel fragment of NXY (see 013727) to yield pDS-NXY. E. coli SG13009 (pUHAT) transformed with pDS-NXY produces a 69 kD fusion protein comprising the NXY	PA	(UNIW) Washington State University.	
CC	units, and C-terminally to a vector-derived sequence.	PI	McGuire TC, Palmer GH, Barbett AF, Davis MC, Allred DR.	
CC	fragment B corresponds to amino acids 1-462 of the N-terminal of the sporozoite antigen. The affinity peptide is used for the purification of the antigen. The polypeptide is useful for the prodn. of antimalarial vaccines.	DR	WPI; 90-313801/44.	
CC	See also 013727-8.	DR	N-PADB; Q07041.	
CC	Sequence 493 AA;	PT	Rickettsial antigens for vaccination and diagnosis - comprise	
CC	Best local Similarity 21.6%; Pred. No. 1.95e-01; Length 493; Matches 16; Conservative 19; Mismatches 38; Indels 1; Gaps 1;	PT	specified amino acid sequences derived from purified surface	
Db	5 hhbbhbgsynsynkennnnkknnkvavkhinavdkvavnkvnkvnktvsklav 64	PS	proteins of Anaplasma marginale.	
OS	: : :::: : : ; : ; ::	CC	Antigens raised to the repeated peptide epitopes encoded by the DNA	
QY	7 HHHHHHSQGHDDDKHKMKKISSVIAIALFGTTATANAADLTASITATATIVEPARITLT 66	CC	preferred are peptides from the following sequence which include the peptide in parentheses:	
Db	65 ykvns-vhkmnavn 77	CC	ADSSASGQEQESSVSQS-[EASTSS]-QLG	
Qy	67 YKEGAPITMDNGN 80	CC	See also R08401-R08405.	
RESULT	12	SQ	Sequence 708 AA;	
ID	R72826 standard; Protein; 2482 AA.	CC		
AC	ACR72826;	CC		
DT	27-FEB-1996 (first entry)	CC		
DE	Human mitosin.	CC		
KW	Cell cycle; M phase; mitosin; retinoblastome; mitosis; cell growth; inhibition.	CC		
OS	Homo sapiens.	CC		
FH	Location/Qualifiers	CC		
FT	Region 1480..1659	CC		
FT	/label= internal_repeat	CC		
FT	Region 1660..1839	CC		
FT	/label= internal_repeat	CC		
FT	W09511309-A2.	CC		
PN		CC		
PD	27-APR-1995.	CC		
PF	24-OCT-1994; US141239.	CC		
PR	22-OCT-1994; US141239.	CC		
PA	(TEXA) UNIV TEXAS SYSTEM.	CC		
PI	Lee W, Zhu X;	CC		
DR	DR	CC		
N-PSDB;	Q86851.	PT	Region	162..166
PT	purified mammalian protein mitosin and agents that bind it and	FT	/Label= conserved sequence in RU6	
PT	inhibit its action - used to promote cell growth or to inhibit cell	FT	Region	647..651
PT	division and/or proliferation	FT	/Label= conserved sequence	
PT	Claim 4; Fig 8B; 61pp; English.	FT	/note= "homologous to sequences	
PS	R72829 is human mitosin. Mitosin is involved in the regulation of	PN	WO9103030-A.	
CC	the mammalian mitotic cell cycle. Mitosin as with E2F-1 (see R72824)	PD	18-OCT-1990; U01678.	
CC	interacts with the retinoblastoma protein (the retinoblastoma tumour	PR	30-MAR-1990.	
CC	suppressor gene product). Mitosin is first synthesised at the G1/S	FT	06-APR-189; US-335178.	
CC	boundary, it is then phosphorylated from S through M phase, and during	FT	(UNIW) Washington State University.	
CC	mitosis, is closely associated with the centromeres/kinetochores at the	FT	McGuire TC, Palmer GH, Barbett AF, Davis MC, Allred DR.	
CC	enter the M phase of the mitotic cell cycle and its degradation is	DR	WPI; 90-313801/44.	
CC	necessary for a cell to advance on to the next stage. Mitosin is thus	DR	N-PADB; Q07041.	
CC	useful for controlling cell growth as overexpression of mitosin prevents	PT	Rickettsial antigens for vaccination and diagnosis - comprise	

CC oligonucleotide probe was synthesized and used to identify DNA
CC encoding the 30 kd protein in a low-passage virulent B. burgdorferi
CC DNA library.
SQ Sequence 257 AA;

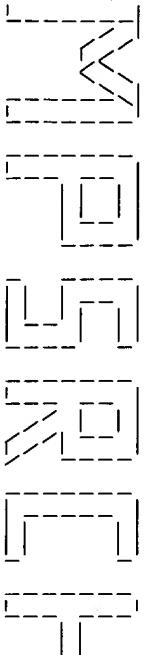
RESULT R13139; standard; Protein; 663 AA.
ID R13139;
AC R13139;
DT 27-SEP-1991 (first entry)
DE B.burgdorferi strain PKO p100 gene;
KW lyme borreliosis; vaccine; flagellin; ss.
OS Borrelia burgdorferi.
PN WO910870-A.
PD 11-JUL-1991.
PF 21-DEC-1990; E0282.
PR 22-DEC-1989; DE-942728.
PR 13-JUN-1990; DE-018988.
PA (MIKR-) MIKROGEN MOLEKULARB.
PI Fuchs R, Wiliske B, Preac-Mursic V, Motz M, Soutschek E.
DR WPI: 91-222844-30.
PT New *Borrelia burgdorferi* proteins - useful as immunoassay
PT reagents and antigens for vaccine prodn.
PS Claim 11; Page 49; 68pp; German.
CC protein p100 was isolated from a *B.burgdorferi* cell lysate and the N-terminal amino acid sequence was determined. A probe pool was
CC synthesised and used to screen a *B.burgdorferi* cDNA library. A clone
CC contg. the 5'-346 nucleotides of the p100 coding sequence was
CC identified and sequenced. Cloning the entire gene allowed the p100
CC amino acid sequence to be deduced.
CC See also 012741-012747, Q13297-8 and R13140-R13142.
Sequence 663 AA;

Best local Similarity 18.3%; Pred. No. 2.55e+01; Matches 19; Conservative 33; Mismatches 48; Indels 4; Gaps 3;

Db	233	qgethdkdtkdielanjheadsnttienlrdqlekatdeehkiesqvadakkq	2922
Oy	416	ORTIQVGSEKKIVSKDFLEGENKRIGALGNKNSSYNKNELSHATTCSDKSRPL	475
Db	293	eel-dkkaidkaqqkldfaendl--igr-dtvrekilgenin	332
Oy	476	NDLVSQTQSDITSRPNSAEALNRPQKDSVMRLDDDS	519

Search completed: Fri Apr 25 12:05:22 1997
Job time : 56 secs.




 (TM)

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 12:02:44 1997; MasPar time 18.34 Seconds
 809.706 Million cell updates/sec

Tabular output not generated.

Title: >US-08-699-716A-2

Description: (1-521) from US08699716A.Pep

Sequence: 1 MGHHHHHHHHSGGHDD.....RFIQKYD SVMQRLLDDTSGK 521

Scoring table: PAM 150

Gap 11

Searched: 89912 seqs, 28507787 residues

post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

pir50
 1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
 13:unann9 14:unann10 15:unenc 16:unrev

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Pred. No.
1	224.5	63.3	326	9 B33601	1
2	212.2	61.8	326	9 B37314	1
3	110.0	31.0	170	9 S13008	1
4	168.4	4.7	168	13 P58315	1
5	127.6	3.6	168	9 S07904	1
6	127.3	3.6	116	11 S57382	1
7	123.5	3.5	168	9 A34952	1
8	123.5	4.89	847608	actin homolog YIL081	1
9	124.3	3.5	857	12 S33821	1
10	123.3	3.5	2076	12 S15999	1
11	120.4	3.4	202	11 S48450	1
12	120.3	3.4	333	1 KIBY450	1
13	121.3	3.4	411	14 L58156	1
14	119.4	3.4	2529	12 A56923	1
15	119.3	3.4	2578	12 A56922	1
16	118.3	3.3	264	13 S34121	1
17	118.3	3.3	410	13 I38502	1
18	116.5	3.3	514181	gene Brn-3b protein	1
19	117.3	3.3	1302	16 JCC6009	1
20	115.3	3.2	812	11 A46417	1
21	111.3	3.1	311	12 S25163	1

RESULT	1	ALIGNMENTS
ENTRY	B33601	
TITLE	Icrv protein #type complete	
ORGANISM	_Yersinia pestis	
DATE	17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change	
ACCESSIONS	B33601	
REFERENCE	A33601	
#authors	Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C.	
#journal	J. Bacteriol. (1989) 171:5645-5653	
#title	Molecular analysis of IcrvGH, the V antigen operon of Yersinia pestis.	
#cross-references	MUID:9008806	
#status	preliminary	
#molecule_type	DNA	
#residues	1-326 #label PRI	
#cross-references	GB:MB0405	
SUMMARY		
Query	Match	63.3%; Score 2245; DB 9; Length 326;
Best Local Similarity	99.4%; Pred. No. 9	45e-282;
Matches	324; Conservative	2; Mismatches 0; Indels 0; Gaps 0;
Db	1 mirayeqnpqfiedekrvrqeqltghgssyleelvqlvkdknidiskpdksevfa	60
Qy	196 MIRAYEQNPQFIEDEKRVQRQLTGHGSSYLEELVQLVKDKNIDISKPDKSEVFA	255
Db	61 nvitddielkkilayfpedaiksgghyqnlqngikrkvkeflessptqweirafma	120
Qy	256 NVITDDIELKKILAYFPEDEIILKGHGDNQLQNGIKRKEFLESSPTQWEIRAFMA	315
Db	121 vnhfsltadiddvvkqvdsmhgdarksklreelaetaelkiyvsiqaeinkhs	180
Qy	316 VNHFSLTADIDDLKVVDMSMHGDARKSKLREELAEALKIYVSIQAEINKHS	375
Db	181 sgtinhdksnlmndknygtdefkasaeylekmpqtigdggsskkirkdf	240
Qy	376 SGTINHDKSNLMNDKNLYGTDEFKASAEYLEKMPQTIGDGGSSKKIRKDF	435
Db	241 gseknrtgalnlnksysynkdnelshtatcdslsrplndlvsaqttsldtsrns	300
Qy	436 GSEKNRTGALNLNSYSYNKDNEELSHATCDTSRPLNDLVSAQTTSLDSRNS	495

```

QY 496 ALEALNRFIQKYDSVMWORLDDBNSKGK 521

#cross-references EMBL:X61996
GENETICS
#gene cafl
FEATURE
#product capsular antigen F1 #status experimental #label SIG\

RESULT 2
ENTRY B37314 #type complete
TITLE regulatory protein LcrV - Yersinia pseudotuberculosis
ORGANISM #formal_name Yersinia pseudotuberculosis
DATE 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change
17-Feb-1994
ACCESSIONS B37314
REFERENCE #authors Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Madelano, A.; Beckman, A.; Boelin, I.; Wolf-Watz, H.
#journal J. Bacteriol. (1991) 173:1607-1616
#title Analysis of the V antigen lcrGWh-yOPB operon of Yersinia pseudotuberculosis: evidence for a regulatory role of lcrH and lcrV.
SUMMARY #accession B37314
#status preliminary
##molecule_type DNA
##residues 1-326 ##label BER
##cross-references GB:MS7893
#length 326 #molecular-weight 37336 #checksum 4689

Query Match
Best Local Similarity 61.8%; Score 2192; DB 9; Length 326;
Matches 315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Pred. No. 2.08e-274; #text_change

Db 1 mirayeqnphiedekvrvqeqltggsvisveelqvkvdknidskydprkdvfa 60
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 196 MIRAYEQNPHIEDEKVRVQEQLTGGGSVISVEELQVKVDKNIDSKYDPRKDVFA 255
Db 61 nrvidaiellkkileyfpedailkgghdqqlqnqikrkvreflesptwelafrma 120
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 256 NRVIDAIELLKKILEYFPEDAILKGHDQQLQNQIKRKVREFLESPTWELAFMA 315
Db 121 vifhsitadrladdilkvvdmmnhbdarskireelaettkelkisvdaeinhhis 180
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 316 VWHFSLTADRIDDILKIVVDMMNHBDARSKIREELAETTKELKISVDAEINHLS 375
Db 181 gggtinlhdksnlmkdkglygydeeiakasaevkilekmpqtqiegetekkvisknf 240
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 376 SGTTINLHKDSKINMDKNGYDDEIFKRASAEVYKILERMPQTQIQQDSEKKIVSKDF 435
Db 241 esekktgaalgnlkdsyksnkaneshattcsdksrplndlvsqktqlsdisrtfns 300
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 436 GSENKRKGALGNKNSYNSKNNELSFATCSDRSRPLNDLVSQTTQLDITSRENS 495
Db 301 aiealnrfiqkydsvalldatsgk 326
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 496 AIEALNRFIQKYDSVMORLDDBNSKGK 521

RESULT 3
ENTRY S13008 #type complete
TITLE capsular antigen F1 precursor - Yersinia pestis
ORGANISM #formal_name Yersinia pestis
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
18-Jun-1993
ACCESSIONS S13008; S23725
REFERENCE #authors Gal'yov, E. E.; Smirnov, O. Y.; Karlishev, A. V.; Volkovoy, K. I.; Denesyuk, A. I.; Nazimov, I. V.; Rubtsov, K. S.; Abramov, V. M.; Dalvadzran, S. M.; Zav'yalov, V. P.
#journal FEBS Lett. (1990) 277:230-232
#title Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative I and B cell epitopes.
#cross-references MUID:91099503
#molecule-type DNA
#residues 1-170 ##label GAL
#accession S13008
##molecule-type DNA
#residues 1-170 ##label GAL

#cross-references EMBL:X61995
GENETICS
#status preliminary
RESULT 4
ENTRY I58315 #type complete
TITLE WT1 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I58315
REFERENCE #authors Hamilton, T. B.; Barilla, R. C.; Romanuk, P. J.
#journal Nucleic Acids Res. (1995) 23:277-284
#title High affinity binding sites for the Wilms' tumour suppressor protein WT1.
#cross-references MUID:95166649
#accession I58315
#status preliminary: translated from GB/EMBL/DDJB
#molecule_type mRNA
#residues 1-168 ##label RES
##cross-references GB:S75264; MUID:9896246; CDS_PID:9896247
GENETICS
#note gene name WT1
#residues 1-168 ##label RES
##cross-references GB:S75264; MUID:9896246; CDS_PID:9896247
#length 168 #molecular-weight 20165 #checksum 6457
SUMMARY
Query Match
Best Local Similarity 4.7%; Score 168; DB 13; Length 168;
Matches 20; Conservative 7; Mismatches 1; Indels 2; Gaps 1;
Pred. No. 4.08e-05; #text_change

Db 1 mghhhhhhhhhhhhsshg-h-rhmrrpgv 28
|||||||l|||||l|||||l|||||l|||||l|||||l|||||l|||||l
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
QY 1 MGHHHHHHHHHHSSGHIDDDKMKKLUSS 30

RESULT 5
ENTRY S07904 #type complete
TITLE CS3 pilin precursor - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S07904
REFERENCE #authors Jalajkumari, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A.; Mol. Microbiol. (1989) 3:1685-1695
#title Genes for biosynthesis and assembly of CS3 pili of CFA/VII enterotoxigenic Escherichia coli: novel regulation of pilus production by bypassing an amber codon.
#cross-references MUID:90158116
#accession S07904
#status preliminary

```

```

##molecule_type DNA
##residues 1-168 ##label JAL
##cross-references EMBL:X16944
#length 168 #molecular-weight 17491 #checksum 8973
SUMMARY
Query Match 3.6%; Score 127; DB 9; Length 168;
Best Local Similarity 24.1%; Pred. No. 3.73e-01; Mismatches 72; Indels 10; Gaps 10;
Matches 41; Conservative 47; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlkikyilglislsamsyslaagptlkkelalnvlspaldatwapqdnltstg-v 59
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 24 MKISSV-IARLFGIA-TANRADITASTATATIVEPARLTIREGAPITIMDGNI 81
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 -sntlygvltntsidsvlastnvsdtskqgt-vtfahetnsasfatt-istdnani 116
| : | | | : | | : | : | : | : | : | : | : | : | : | : | : |
Qy 82 DIELLVGLTLLGGYKGTTS-TSVNFTDAAGDPWMLTFTSDGNHHOFTTKVIGKDSRDF 140
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 117 tld-knagntriv-kttngsqlpnlpkfittegnehlvsgnyranit 164
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 141 DISPKVNGENLVGDDVVLAUTGSQDFFFVRSIGSKGGK-LAAGKTYDAVTVT 189

RESULT 6
ENTRY S57382 #type complete
TITLE hypothetical protein YOL087c - yeast (Saccharomyces cerevisiae)
ALTERNATE NAMES hypothetical protein 00944
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
02-Aug-1996
S57382; S56781; S50418
S57374; Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

#journal Yeast (1995) 11:975-986
#title A 29.42 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.

#accession S57382
#status nucleic acid sequence not shown
#molecule_type DNA
##residues 1-116 ##label ZUM
REFERENCE S56775 Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
#authors submitted to the Protein Sequence Database, July 1996
#submission EMBL:XB3121
#cross-references EMBL:XB3121
#GENETICS #map_position 15L
#molecule_type DNA
##residues 1-116 ##label ZUW
##cross-references EMBL:Z74829
##experimental_source strain S288C
SUMMARY
Query Match 3.6%; Score 127; DB 11; Length 116;
Best Local Similarity 47.1%; Pred. No. 3.73e-01; Mismatches 16; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Db 365 hhhhhhhhheheeqnnsttakvkyggdiall 398
| | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 3 HHHHHHHHHSSGHDDDKHMKKISSVIALF 36
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 7
ENTRY A34952 #type complete
TITLE CS3 fimbrial Protein precursor - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
04-Nov-1994
ACCESSIONS A34952
REFERENCE A34952

RESULT 8
ENTRY S47508 #type complete
TITLE actin homolog YJLBIC - Yeast (Saccharomyces cerevisiae)
ALTERNATE NAMES protein J1012; protein YJLBIC
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
08-Sep-1995
S47508; S56029; S55858; S37563
REFERENCE S47508
#authors Wintersberger, U.
#submission submitted to the EMBL Data Library, December 1993
#accession S47608
#molecule_type DNA
##residues 1-469 ##label WIN
#cross-references EMBL:X75317
REFERENCE S556016
#authors Misoga, T.; Schaaff-Gerstenschlaeger, I.; Chalwatzis, N.; Baur, A.; Boles, E.; Fournier, C.; Schmitt, S.; Veltén, C.; Wilhelm, N.; Zimmermann, F.K.
#journal Yeast (1995) 11:681-689
#title Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)(2)-Cys(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.
#accession S556029
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
##residues 1-469 ##label MIO
##cross-references EMBL:XB3502
#note the nucleotide sequence was submitted to the EMBL Data Library, December 1994
REFERENCE S55685
#authors Misoga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournier, C.; Schmitt, S.; Veltén, C.; Wilhelm, N.; Witzel, A.; Zimmermann, F.K.
#submission submitted to the Protein Sequence Database, September 1995
#accession S55685
#molecule_type DNA
##residues 1-489 ##label MIW

```

GENETICS ##cross-references EMBL:Z49356
 #gene ACT3
 #map_position 10L
 CLASSIFICATION #superfamily actin
 #length 489 #molecular-weight 54831 #checksum 8019
 Query Match 3.5%; Score 123; DB 7; Length 489;
 Best Local Similarity 25.8%; Pred. No. 8.48e-01; Gaps 1;
 Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;
 #residues 1-2076 ##label MOU
 #cross-references EMBL:X59690
 GENETICS FAS1
 #gene acyltransferase
 #molecule_type DNA
 #length 2076 #molecular-weight 230223 #checksum 5483
 Query Match 3.5%; Score 123; DB 12; Length 2076;
 Best Local Similarity 31.3%; Pred. No. 8.48e-01; Gaps 5;
 Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5;
 #residues 1-1995 ##label SPKVNNGENLV 152
 Db 22 gsytrringysgsdfqsgspsvgyktadegnkifseqsgiprkyelkpiae-nly 80
 Qy 93 GGYKTGTTSTSVNFTDAAGDPMLTFTSODGNHQTTKVIGKDSRDFDISPKVNNGENLV 152
 Db 81 id 82
 Qy 153 GD 154

RESULT 9
 ENTRY S33821 #type complete
 TITLE median body protein - Giardia lamblia
 ORGANISM #formal_name Giardia lamblia
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
 ACCESSIONS S33821
 REFERENCE Marshall, J.; Holberton, D.V.
 #authors J.Mol. Biol. (1993) 231:521-530
 #journal Sequence and structure of a new coiled coil protein from a microtubule bundle in Giardia.
 #accession S33821
 #status preliminary
 #molecule-type mRNA
 #residues 1-857 ##label MAR
 SUMMARY #length 857 #molecular-weight 100583 #checksum 6805
 Query Match 3.5%; Score 124; DB 12; Length 857;
 Best Local Similarity 20.1%; Pred. No. 6.92e-01; Gaps 17;
 Matches 43; Conservative 71; Mismatches 82; Indels 18; Gaps 17;
 ACCESSIONS S48450
 REFERENCE Rowley, N.
 #authors submitted to the EMBL Data Library, August 1994
 #accession S48450
 #molecule-type DNA
 #residues 1-220 ##label ROW
 #cross-references EMBL:Z38113
 GENETICS
 #map_position 9L
 #length 220 #molecular-weight 24846 #checksum 3126
 Query Match 3.4%; Score 120; DB 11; Length 220;
 Best Local Similarity 22.8%; Pred. No. 1.56e-01; Gaps 7;
 Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7;
 #residues 1-111 ##label ROW
 Db 38 ktdietqleay-fsvlqeaggg-igmdsalvtpdgy-prsadvdvlqvttmrkknvmlndl 94
 Qy 262 DIELK-KILAYF-IPEDTILKGHDYDNLONGIKRV-K-EFLESSPNTQ-WELRA-FMA 315
 Db 701 vdtlveekqplemaelkikvnnyqladdkar-qeqklkmsdkiefemimdd-nrrl 759
 Qy 316 VMHFSLTADRIDDI--LKVIYDPMNHGDKRSKREELALTAELAKIYVIAEINKHL 373
 Db 760 klqvk-eldiktan-mek-lyyeeykkledqklat 790
 Qy 374 SSSGTINIHDXSINLMDKNLYG-YTD-EEIFKAS 405

RESULT 10
 ENTRY S15999 #type complete
 TITLE fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast
 (Yarrowia lipolytica)
 ORGANISM #formal_name Yarrowia lipolytica, Candida lipolytica
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
 11-Jun-1993
 #authors Schweißer, E.; Schweizer, M.; Koettig, H.; Rottnér, G.; Beck, K.F.; Schweizer, M.; Mol. Genet. (1991) 226:310-314
 #journal The pentafunctional FAS1 genes of *Saccharomyces cerevisiae*

RESULT 11
 ENTRY S48450 #type complete
 TITLE hypothetical protein YIL007c - yeast (Saccharomyces cerevisiae)
 ORGANISM #formal_name Saccharomyces cerevisiae
 DATE 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
 01-Mar-1996
 ACCESSIONS S48450
 REFERENCE Rowley, N.
 #authors submitted to the EMBL Data Library, August 1994
 #accession S48450
 #molecule-type DNA
 #residues 1-220 ##label ROW
 #cross-references EMBL:Z38113
 GENETICS
 #map_position 9L
 #length 220 #molecular-weight 24846 #checksum 3126
 Query Match 3.4%; Score 120; DB 11; Length 220;
 Best Local Similarity 22.8%; Pred. No. 1.56e-01; Gaps 7;
 Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7;
 #residues 1-111 ##label ROW
 Db 38 ktdietqleay-fsvlqeaggg-igmdsalvtpdgy-prsadvdvlqvttmrkknvmlndl 94
 Qy 213 KVRE-QLIGHGGSYLEEVQVLDKNTNISIKDPRKSEVFANRVITDDIELUKTLA 271
 Db 95 hilqrshvnlqhqfamnvsngdarrn-ddcaiqytptfafisevprgspsdakiv 153
 Qy 272 YFLPEDTILKGHDYDNLONGIKRVKEFLESSPNTQWELR-AFMAVMHSLTADRIDDI 330
 Db 154 ddklisignvhaapbsklpglqmvvmke 182
 Qy 331 LKVIVDSMNHHGDARSKLR-EELATAE 358

RESULT 12
 ENTRY KIBYRB #type complete
 TITLE ribokinase (EC 2.7.1.15) - yeast (Saccharomyces cerevisiae)
 ALTERNATE NAMES protein YCR036w; protein YCR523
 ORGANISM #formal_name *Saccharomyces cerevisiae*
 DATE 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
 23-Aug-1996
 ACCESSIONS S12918; S12916
 REFERENCE
 #authors Thierry, A.; Fairhead, C.; Dujon, B.
 #journal Yeast (1990) 6:521-534
 #title The complete sequence of the 8.2 kb segment left of MAT on

#cross-references chromosome III reveals five ORFs, including a gene for a yeast ribokinase. MUID:91181345.

REFERENCE Sl9445
#authors Herpert, C.J.; Jia, Y.; Sloninski, P.P.
#submission submitted to the Protein Sequence database, March 1992
#accession S19448
##molecule_type DNA
##residues 1-333 #!label DUJ
##cross-references EMBL:X56909

REFERENCE A56923
#authors Glieder, N.C.; Neilen, D.; Burke, R.; Basler, K.; Affolter, M.
#journal Cell (1995) 81:791-800
#title schnurri is required for Drosophila Dpp signaling and encodes a zinc finger protein similar to the mammalian transcription factor PRDII-BF1.

REFERENCE A56923
#journal Cell (1995) 81:791-800
#text_change 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 25-May-1996

ACCESSIONS

ORGANISM schnurri

KEYWORDS yeast ribokinase

GENETICS

ENTRY RBKL
#gene RBKL
#map_position 3R
#superfamily ribokinase

SUMMARY

Query Match 3.4%; Score 120; DB 1; Length 333;
Best Local Similarity 23.2%; Pred. No. 1.35e+00;
Matches 22; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

Query Match 3.4%; Score 119; DB 12; Length 2529;
Best Local Similarity 24.6%; Pred. No. 1.90e+00;
Matches 32; Conservative 38; Mismatches 55; Indels 5; Gaps 5;

Query Match 3.4%; Score 119; DB 12; Length 2529;
Best Local Similarity 24.6%; Pred. No. 1.90e+00;
Matches 32; Conservative 38; Mismatches 55; Indels 5; Gaps 5;

Db 235 Klmnkkrkgivmtlqrgvlfcshepveqfpaigqsvvvttgadtfqglvtly 294
Qy 176 KLAAGKVTDAVTVTVSVNOEFMIRAYEQNPHQFEDLERVVEQLTGHGSSVLELV-QIV 234

Db 295 qgetlsmakffstlassltiqkgaasmplyvdv 329
Qy 235 KDKNIDISIKYDPRKDSEVFANRVITDDILLRKI 269

RESULT 13
#organism mouse
#formal_name MUS SP. #common_name mouse
#text_change 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996

ACCESSIONS

REFERENCE 158156
#authors Turner, E.E.; Jenne, K.J.; Rosenfeld, M.G.
#journal Neuron (1994) 12:205-218
#title Brn-3-2: a Brn-3-related transcription factor with distinctive central nervous system expression and regulation by retinoic acid.

ACCESSION 158156
#status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-411 #!label RES
##cross-references GB:S68377; NID:9545068; CDS_PID:9545069

GENETICS

NOTE gene name Brn-3-2

SUMMARY

Query Match 3.4%; Score 121; DB 14; Length 411;
Best Local Similarity 28.6%; Pred. No. 1.27e+00;
Matches 24; Conservative 22; Mismatches 35; Indels 3; Gaps 3;

Db 174 hhhhhhhhhphphqalegeliehlspalgamagpdgtvstphahbmtnpmhca 233
Qy 3 HHHHHHHHHSCHIDDDKHMKISSVTAI-ALFGTTATANADLTASSTATLVEPA 61

Db 234 alsmahqglp-shmgcnsdva 256
Qy 62 RTILTYE6GAPTMIDNGNIDIE 84

RESULT 14
#entry RESULT
#title A56923
#text_change 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 25-May-1996

ACCESSIONS

ORGANISM Drosophila melanogaster

KEYWORDS schnurri

GENETICS

ENTRY LATGSQDFEV
#organism Drosophila melanogaster
#formal_name Drosophila melanogaster
#text_change 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 25-May-1996

ACCESSIONS

REFERENCE A56922
#authors Letson, A.; Warrior, R.
#journal Cell (1995) 81:781-790
#title The Drosophila schnurri gene acts in the Dpp/TGFbeta signaling pathway and encodes a transcription factor homologous to the human MBP family.

ACCESSION A56922
#status preliminary; nucleic acid sequence not shown; not compared with conceptual translation

SUMMARY

Query Match 3.4%; Score 119; DB 12; Length 2578;
Best Local Similarity 24.6%; Pred. No. 1.90e+00;
Matches 32; Conservative 38; Mismatches 55; Indels 5; Gaps 5;

Query Match 3.4%; Score 119; DB 12; Length 2578;
Best Local Similarity 24.6%; Pred. No. 1.90e+00;
Matches 32; Conservative 38; Mismatches 55; Indels 5; Gaps 5;

Db 80 ataaaaaaaatvttaatptkkr-tvreataattvlgqrstkaniaaalaaate 138
Qy 38 TIATANADLTASSTATLVEPARTILYREGATPTIMDGNDTPEELLYGLTGT 97

Db 139 atassasatataat-lt-askaaataattdaasgnsskshtsrdrkl-ge-vp 194
Qy 98 GTTSFSVNFDTAAGPMWLTTSQDGNNHQFTTKVIGKDSRDFDPSPKVNGENLVSDVV 157

Db 195 lptvsnhil 204

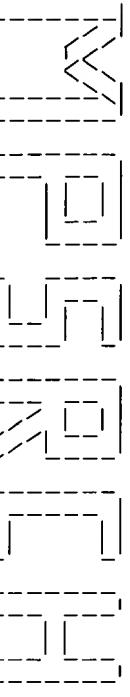
Mon Apr 28 07:53:51 1997

US-08-699-716A-2.rpr

Page 6

QY | :| : ::
158 LATGSDFFV 167

Search completed: Fri Apr 25 12:04:07 1997
Job time : 83 secs.


 (TM)

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MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Apr 25 12:01:35 1997; MasPar time 13.01 Seconds
 Tabular output not generated.

Title:

>US-08-699-716A-2
(1-521) from US08699716A.pep

Description:

Perfect Score:

Sequence:

PAM 150

Scoring table:
 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0 & summaries

Database: swiss-prot34
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 53.350; Variance 126.457; scale 0.422

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	Pred. No.
1	2245	63.3	326	5	LCRV_YERPE	VIRULENCE-ASSOCIATED
2	2192	61.8	326	5	LCRV_YERPE	VIRULENCE-ASSOCIATED
3	1100	31.0	170	2	CAPF_ECOLI	FL CAPSULE ANTIGEN PR
4	127	3.6	168	4	FMS1_ECOLI	CS3 FIMBRIAL SUBUNIT
5	123	3.5	489	1	ACT3_YEAST	ACTIN-LIKE PROTEIN AC
6	124	3.5	857	6	MED1_GILA	MEDIAN BODY PROTEIN.
7	123	3.5	2076	3	FASL_YARLI	FATTY ACID SYNTHASE,
8	120	3.4	220	11	Y1AY1_YEAST	HYPOTHETICAL 24.8 KD
9	120	3.4	333	8	PTA_HAETN	PROBABLE RIBONUCLEIC ACYLTRANSFERASE
10	115	3.2	812	6	NPI1_YEAST	NUCLEAR TRANSPORT PRO
11	112	3.2	973	2	COPB_YEAST	COTOMER BETA SUBUNIT
12	109	3.1	173	4	HA31_BGLC	HAM3 PROTEIN.
13	111	3.1	311	4	GIAG_GIALA	GIARDIN GAMMA CHAIN.
14	110	3.1	558	8	RECN_HAETN	DNA REPAIR PROTEIN RE
15	109	3.1	710	8	PTA_HAETN	PHOSPHATE ACYLTRANS
16	110	3.1	835	5	INVA_YEREN	INVASIN.
17	109	3.1	982	7	P115_MYCGE	P115 PROTEIN HOMOLOG.
18	111	3.1	1004	9	SLPO_CELL	OUTER CELL WALL PROTE
19	106	3.0	258	6	NCAP_ISWV3	NUCLEOCAPSID PROTEIN.
20	106	3.0	361	5	HYPB_ALCEU	HYDROGENASE EXPRESIO
21	106	3.0	375	2	CAR2_DICDU	CYCLOC AMP RECEPTOR 2
22	108	3.0	455	7	NUBR2_MOUSE	NUCLEOBINDIN PRECURSO

RESULT ID	1 LCRV_YERPE	STANDARD; PRT;	326 AA.
AC P21206;	01-MAY-1991 (REL. 18, CREATED)		
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)			
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)			
DE VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN DE V).			
DR YERSINTIA PESTIS.			
OG PLASMID PCD1.			
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=KIM;			
RX MEDLINE; 90008806.			
RA PRICE S.B., LEUNG K.Y., BARVE S.S., STRALEY S.C.;			
RL J. BACTERIOL. 171:5646-5653(1989).			
CC SEQUENCE FROM N.A.			
CC -1- SUBCELLULAR LOCATION: SECRETED.			
DR EMBL; M26405; G155450; ALT_SEQ.			
DR PIR; B33601; B33601.			
KW SEQUENCE; ANTIGEN; VIRULENCE.			
SO QUERY MATCH			
Best Local Similarity 99.4%; Pred. No. 0 0.0e+00;			
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
DB 1 mirayegnpgifedekvrgveqltgghgsasleelvqlvknidiskikprksevfa 60			
QY 196 MIRAYEGNPGIFEDEKVRGVEQLTGHHGSASLEELVQLVKNDISKIKPRKSEVFA 255			
DB 61 nrvitdileikkilaypledaikgghndqlqngikvkfiesptqwgelrafma 120			
QY 316 WMRSLTADRIDDIKVIVDSMNKHGDAKSRELAETRAELKIVSYQREINHLSS 375			
DB 181 sqtinhdksnlmdknlyyydefkaaaeykilekmqgqticvdgsskkivskdf 240			
QY 376 SGTTINHDKSINLMDKNLYYYDEFKAAYKILEKMPQTICVDGSSKKIVSKDF 435			

Db	241	gseckrtgalgnlknsysynkdnnelshfattcsdksrplndivsqtktsqldtsrfns	300	DE F1 CAPSULE ANTIGEN PRECURSOR.
				GN CAFI.
Qy	436	GSECKRTGALGNLKNSYSYNKDNNELSHFATTCSDKSRPLNDIVSQTKTSQLDTSRFNS	495	GN YERSINIA PESTIS.
Db	301	aiealnrfiqkyddvngmrlddtsgk	326	OS PLASMID PERA.
Qy	496	AIEALNRFIQKYDDVNGMRLDTSRGK	521	OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.
RESULT	2			[1]
ID	LCRY-YEPRS	STANDARD:	PRT:	RP
AC	P2394;			RX
DT	01-MAR-1992 (REL. 21, CREATED)			RA
DT	01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)			RA
DT	01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)			DALVADYANZ S.M., ZAV'YAOV V.P.;
DE	VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V).			CC SUBCELLULAR LOCATION: CAPSULE.
DE	LCRY.			DR EMBL: X61996; G48621; -.
GN	VERSINIA PSEUDOTUBERCULOSIS.			DR PIR: S13008; S13008.
OS	PLASMID PPI1.			KW PLASMID; SIGNAL:
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			FT SIGNAL 1 21 POTENTIAL.
RN	[1]			FT CHAIN 22 170 F1 CAPSULE ANTIGEN.
RP	SEQUENCE FROM N.A.			FT DOMAIN 100 150 CONTAINS POTENTIAL ANTIGENIC DETERMINANTS THAT MAY STIMULATE T-CELLS.
RC	STRAIN=PP1;			FT FT
RC	MEDLINE; 91154114.			FT SEQUENCE 170 AA; 17666 MW; 3543225 CRC32;
RA	BERGMAN T., HANSSON S., FORSSBERG A., NORLANDER L., MACELLARO A., BRECKMAN A., BOELIN T., WOLF-WATZ H.;			QY
RA	J. BACTERIOL. 173:1607-1616(1991).			Db 1 mkkissvvialfytiaanaditasstataatveparitlykegapitindngndt 60
RL	-!!- FUNCTION: INVOLVED IN CA(+) REGULATION OF YOP EXPRESSION, WHICH INCLUDES THE EXPORT PROCESS.			Qy 24 MKKISSVIALFYTIAANADITASSTATAATVEPARITLYKEGAPITINDNGNDT 83
CC	-!!- SUBCELLULAR LOCATION: SECRETED.			Db 61 elvgltlgtgyktgtstsavnftdaaqdpmyltfsedgnnhqfttkvlgksrdfls 120
CC	-!!- SUBCELLULAR LOCATION: SECRETED.			Qy 84 ELVGTLGTGKGRTTSVSNFTDAQDPMYLTFSQDGNHQQFTTKVIGKOSRFDIS 143
DR	EMBL: M57893; G155458; -.			Db 121 pkvngenvgddvrlatgsqdfvrsqskggklaagkytdavtvysq 170
DR	PIR; B37314; B37314;			Qy 144 PKVNGENVGDDVVRLATGSQDFVRSIGSKGGKLAAGYTDATVTVVSNO 193
KW	PLASMID; ANTIGEN; VIRULENCE.			
SQ	SEQUENCE 326 AA; 37336 MW; 7D94E243 CRC32;			
Query Match	61.8%	Score 2192; DB 5; Length 326;		
Best Local Similarity	96.6%	Pred. No. 0 00e-00; Indels 0; Gaps 0;		
Matches	315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;			
RESULT	4			
ID	FMS3-ECOLI	STANDARD:	PRT:	DE
AC	P1548;			GN F1 CAPSULE ANTIGEN PRECURSOR.
AC	01-APR-1990 (REL. 14, CREATED)			GN CAFI.
DT	01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)			GN YERSINIA PESTIS.
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			OS PLASMID PERA.
DE	C33 FIMBRIAL SUBUNIT A PRECURSOR (C33 PILIN).			OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.
OS	ESCHERICHIA COLI.			RC SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC STRAIN=PB176;
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC MEDLINE; 9018116.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC JALAIKUMARI M.B., THOMAS C.J., HALTER R., MANNING P.A.;
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC MOL. MICROBIOL. 3:1685-1695(1989).
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC [2]
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC SEQUENCE FROM N.A.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC MEDLINE; 89036361.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC BOYDIN M., SMITH C.J., SCOTT J.R.;
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC INFECT. IMMUN. 56:3297-3300(1988).
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC MEDLINE; 90036735.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC SEQUENCE OF 23-45.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC STRAIN=EP034A;
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC MEDLINE; 90036735.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC HALL R.H., MANHEW D.R. JR., COLLINS J.H., THETBERT J.L., LEVINE M.M.;
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC J. BACTERIOL. 171:6372-6374(1989).
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC -!!- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; OC ENTEROBACTERIACEAE.			RC EMBL; X16944; G41161; -.
DT	01-AUG-1992 (REL. 23, CREATED)			
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)			
DT	01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)			

Query Match 3.4%; Score 120; DB 11; Length 220;
 Best Local Similarity 22.8%; Pred. No. 1.93e-01; Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7;

CC -!- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
 LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 THE BETA SUBUNIT CONTAINS DOMAINS FOR: [ACYL-CARRIER PROTEIN]
 ACETYLTRANSFERASE AND MALONYLTRANSFERASE, S-ACYL FATTY ACID
 SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND
 3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE.

CC -!- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
 LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).

CC -!- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
 LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).

CC -!- CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA
 + ACETYL-[ACYL-CARRIER PROTEIN].

CC -!- CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN] = COA
 + MALONYL-[ACYL-CARRIER PROTEIN].

CC -!- CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
 = 2-HEXADECENOYL-[ACYL-CARRIER PROTEIN] + H(2)O.

CC -!- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = 2,3-
 DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.

CC -!- CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] + H(2)O =
 ACYL-CARRIER PROTEIN + OLATE.

CC -!- SUBUNITS: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)] HEXAMERS OF
 TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).

DR EMBL: X59590; G297785; .

DR PIR: S15939; S15999.

KW FATTY ACID BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME; OXIDOREDUCTASE;

KW TRANSFERASE; HYDROLASE; LIGASE; NAD; NADP.

FT DOMAIN 1 470 ACETYL TRANSFERASE.

FT DOMAIN 482 869 ENOL REDUCTASE.

FT DOMAIN 1156 1647 DEHYDRATASE.

FT DOMAIN 1648 1869 MALONYL/PALMITOYL TRANSFERASE.

FT ACT_SITE 275 276 ACETYL TRANSFERASE (BY SIMILARITY).

FT ACT_SITE 1832 1832 MALONYLTRANSFERASE (BY SIMILARITY).

SQ SEQUENCE 2076 AA; 230223 MW: E10A5234 CRC32;

Query Match 3.5%; Score 123; DB 3; Length 2076;
 Best Local Similarity 31.3%; Pred. No. 9.09e-02; Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5;

Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5;

Db 1268 tdntrnikefkwk1vfgqdkf-felddit-eeliqddvtisgkiaidfhavankgeaf 1325

Qy 119 TSQDGNNHOFTKV-IGKSDRFDISPKVNGENLVGDDVVLTGSQDFVVRSGSKGGKL 177

Db 1326 v-grttsagvv-fapmdfa 1343

Qy 178 AAGKYNDAVTVTVSNOEFMI 197

Query Match 9%; Score 9; DB 9; Length 182;
 Best Local Similarity 22.8%; Pred. No. 1.93e-01; Matches 10; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

CC ID RBSK_YEAST STANDARD; PRT; 333 AA.

AC P25312;

CC DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

CC DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)

CC DE PROBABLE_RBKONKASE (EC 2.7.1.15).
 ON RBK1 OR YCR36W OR YCR52J.

RA OS SACCAROMYCETES_CEREVIAE (BAKER'S YEAST).

RA OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.

RA RN [1] SEQUENCE FROM N.A.

RP RC STRAIN=S288C / FY1679;
 RX MEDLINE; 91181345.

RA RA THIERRY A., FAIRHEAD C., DUJON B.;

CC RL YEAST 6:521-534 (1990).

CC DR EMBL; X56009; G4492; .

CC DR PIR; S12918; KIBYRB.

CC DR LISTA; SC00940; RBKL.

CC DR SGD; L001587; RBKL.

DR PROSITE; PS00583; PFKB_KINASES_1.

DR PROSITE; PS00584; PFKB_KINASES_2.

KW SEQUENCE 333 AA; 36904 MW; 3E1772EC CRC32;

Query Match 3.4%; Score 120; DB 8; Length 333;
 Best Local Similarity 23.2%; Pred. No. 1.93e-01; Matches 22; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

Db 235 klmnkkrkgivmltgsgqylfcshespewqfpaiqnvsvatggdftffgllvta 294

Qy 176 KLAQSKYDTRVPTVSNQFPRMTRAYEQNQHFFDLKRYVEQDGLGSSVLLYQIV 234

Db 295 qgetlsmakfstlassltqrkgaaesnplykd 329

Qy 235 KDKNIDISKYDPRKDSEEVANRVITDDIELKKI 269

Query Match 10%; Score 10; DB 10; Length 800;
 Best Local Similarity 22.8%; Pred. No. 1.93e-01; Matches 10; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

CC ID NIPLYEAST STANDARD; PRT; 812 AA.

AC P3247;

CC DT 01-OCT-1993 (REL. 27, CREATED)

CC DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

CC DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE NUCLEAR TRANSPORT PROTEIN NIP1.

GN NIP1 OR YMR309C OR YM934.01C OR YM952.11C.

OS SACCHAROMYCETES_CEREVIAE (BAKER'S YEAST).

OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.

CC [1] SEQUENCE FROM N.A.

RX MEDLINE; 93066237.

RA GU Z., MOERSCHELL R.P., SHERMAN F., GOLDFARB D.S.;
 PROC. NAIL. ACADEM. SCI. U.S.A. 89:10355-10359(1992).
 RN [12]
 SEQUENCE OF 1-602 FROM N.A.
 RC STRAIN=S2B8C / AB972;
 RC CHURCHER C.M., LOUIS E.J., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RC SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ/NCBI DATA BANKS.
 RN [3]
 SEQUENCE OF 571-812 FROM N.A.
 RP STRAIN=S2B8C / AB972;
 RC CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RC SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ/NCBI DATA BANKS.
 -!- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE NUCLEUS;
 CC PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.
 CC SUBUNIT: MONOMER.
 -!- SUBCELLULAR LOCATION: CYTOPLASMIC; MAINLY.
 DR EMBL: L02899; ; NOT_ANNOTATED_CDS.
 DR EMBL: Z5412; G94682; ;
 DR EMBL: Z49212; G788951; ;
 DR PIR: A46417; A46417.
 DR LISTA; SC00714; NPPI.
 DR SGD; L000122; NPPI.
 KW TRANSPORT; PROTEIN TRANSPORT.
 FT DOMAIN 15 147 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 15 36 SER-RICH.
 FT CONFLICT 111 111 V->D (IN REF. 1).
 FT CONFLICT 583 583 Q->H (IN REF. 1).
 FT CONFLICT 641 641 K->N (IN REF. 1).
 FT CONFLICT 643 643 K->N (IN REF. 1).
 SQ SEQUENCE 812 AA; 93204 MW; 4793DCE CRC32;
 Query Match 3.2%; Score 115; DB 6; Length 812;
 Best Local Similarity 29.2%; Pred. No. 6.54e-01;
 Matches 31; Conservative 28; Mismatches 39; Indels 8; Gaps 8;
 PRT; 973 AA.
 ID HA34_BRELC STANDARD; PRT; 173 AA.
 AC Q99074;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DR HAM34 PROTEIN.
 RC GN BREMIA LACTUCAE (LETTUCE DOWNTWILDEN).
 OC OS EUKARYOTA; FUNGI; MASTIGONYCOTINA; OOMYCETES.
 RN [1]
 SEQUENCE FROM N.A.
 DR RX JUDELSON H.S., MICHELMORE R.W.;
 RL MOL. PLANT MICROBE INTERACT. 3:225-232(1990).
 CC -!- FUNCTION: COULD BE A STRUCTURAL PROTEIN REQUIRED FOR THE
 CC INFECTION PROCESS OF B.LACTUCAE.
 CC -!- TISSUE SPECIFICITY: GERMINATING SPORES.
 DR EMBL; X16984; G2488; ;
 KW SPORULATION; STRUCTURAL PROTEIN.
 SQ SEQUENCE 173 AA; 16478 MW; 43864282 CRC32;
 Query Match 3.1%; Score 109; DB 4; Length 173;
 Best Local Similarity 24.3%; Pred. No. 2.70e+00;
 Matches 28; Conservative 28; Mismatches 58; Indels 1; Gaps 1;
 PRT; 311 AA.
 ID GIAG_GIALA STANDARD; PRT; 311 AA.
 AC P38413;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DR GIARDIN GAMMA CHAIN.
 OC OS GIARDIA LAMBLIA (GIARDIA INTESTINALIS).
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
 OC HEXAMITIDA.
 RN [1]
 SEQUENCE FROM N.A., AND SEQUENCE OF 145-156.
 RP

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Search completed: Fri Apr 25 12:02:27 1997
Job time : 52 secs.



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